

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 18, 2000, 21:02:06 ; Search time 3378.13 Seconds  
(without alignments)  
3935.252 Million cell updates/sec

Title: US-09-303-232-5  
Perfect score: 3109  
Sequence: 1 ggcacgagccgcccgaagt.....ggtaagtgtacccaattggc 3109

Scoring table: IDENTITY\_NUC

Searched: 780561 seqs, 2137953050 residues

Database : GenEmbl.\*

Word size : 0

Number of hits that pass the threshold : 1561122

- 1: gb\_bal.\*
- 2: gb\_bal2.\*
- 3: gb\_ov.\*
- 4: gb\_ov.\*
- 5: gb\_pat.\*
- 6: gb\_ph.\*
- 7: gb\_pl1.\*
- 8: gb\_pl2.\*
- 9: gb\_pr1.\*
- 10: gb\_pr2.\*
- 11: gb\_pr3.\*
- 12: gb\_ro.\*
- 13: gb\_sts.\*
- 14: gb\_sy.\*
- 15: gb\_un.\*
- 16: gb\_v1.\*
- 17: em\_fun.\*
- 18: em\_htg.\*
- 19: em\_hum1.\*
- 20: em\_hum2.\*
- 21: em\_in.\*
- 22: em\_om.\*
- 23: em\_ov.\*
- 24: em\_ov.\*
- 25: em\_pat.\*
- 26: em\_ph.\*
- 27: em\_pl.\*
- 28: em\_ro.\*
- 29: em\_sts.\*
- 30: em\_sy.\*
- 31: em\_un.\*
- 32: em\_v1.\*
- 33: gb\_htg1.\*
- 34: gb\_htg2.\*
- 35: gb\_in1.\*
- 36: gb\_in2.\*
- 37: em\_bal.\*
- 38: em\_bal2.\*
- 39: em\_hum3.\*
- 40: em\_hum4.\*
- 41: gb\_pr4.\*
- 42: gb\_htg3.\*
- 43: gb\_htg4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3029	97.4	3029	36	AF143847
2	579.8	18.6	3629	36	AF143846
3	379.6	12.2	1509	9	HSNACHRA7
4	379.6	12.2	1977	10	HSU40583
5	378	12.2	1551	3	BSA7
6	378	12.2	2087	9	HSARA7A
7	377.4	12.1	1559	10	HUMAYNAR
8	376.4	12.1	1876	11	HSU62436
9	376.4	12.1	2106	12	RATNARAD
10	376.4	12.1	3030	12	S53987
11	376	12.1	1876	5	AR055255
12	374.8	12.1	1848	12	MUSNARS
13	367.4	11.8	1555	9	HSCHRNA7A
14	349	11.2	2037	4	GGNARA7A
15	342.4	11.0	2896	4	GGATNAREC
16	326.8	10.5	2090	4	GGATNAREC
17	305.6	9.8	1512	9	HSNACHRA3A
18	304.4	9.8	1884	9	HSNACHRA4
19	304.4	9.8	3343	11	HSU62433
20	303.2	9.7	1910	10	HUMNAR
21	303	9.7	1833	9	HSNACHRA4G
22	302.8	9.7	2082	10	HUMNACHRA4
23	302.2	9.7	2277	5	AR037435
24	302.2	9.7	1590	10	HSY16281
25	302.2	9.7	2684	11	HSU62431
26	301.8	9.7	1931	12	RATNAR
27	298.8	9.6	1584	41	HUM3NARSP
28	298.2	9.6	2095	12	RATNARAC
29	298.2	9.6	1756	5	AR055253
30	297.6	9.5	2149	12	AF007212
31	296.6	9.5	2327	12	RATNARAB
32	296.4	9.5	1956	3	BTACHRECA
33	296.4	9.5	1425	9	HSNACHRA3
34	291.6	9.4	2374	5	AR055254
35	288	9.3	2374	5	AR055254
36	286.8	9.2	2838	35	DMNARS
37	285.8	9.2	2068	5	AR055252
38	285	9.2	2067	35	HVNACHRA1
39	284.4	9.1	1578	35	LMNACHRA2
40	284.2	9.1	1858	12	RATNARA
41	284.2	9.1	1932	12	RNACHRAR
42	282.2	9.1	1963	35	SGNAAL1
43	281.6	9.1	1700	12	AF145286
44	281.4	9.1	1828	35	CENCHRA1
45	281.2	9.0	2197	12	RATNARB

ALIGNMENTS

RESULT 1

AF143847

LOCUS

DEFINITION

ACCESSION

NID

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AF143847 3029 bp mRNA INV 27-MAY-1999  
Heliothis virescens putative nicotinic acetylcholine receptor alpha  
7-2 subunit mRNA, complete cds.  
AF143847  
GI:4895006  
tobacco budworm.  
Heliothis virescens  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;  
Ditrysia; Noctuidae; Noctuidae; Heliothinae; Heliothis.  
1 (bases 1 to 3029)  
Schulze, T., Oellers, N. and Adamczewski, M.  
Putative alpha subunits of insect nicotinic acetylcholine receptors  
more similar to vertebrate alpha 7 subunits and C. elegans Ce21  
than to other insect nicotinic acetylcholine receptor alpha



Db	1621	CTCGGCGCATGAATGAGAGAAATAATATTATAGATCCCGATTGTGAATTATTAATTGATA	1680
Qy	1681	atgtaataataataaacatcagtgttgaaacgcacacgtctccatacaacaagctcttaagac	1740
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Qy	1741	attaaattatgataaaattacatatctagttaagtcgagtggtgataggaaaatttttagcc	1800
Db	1741	ATTAATATGATAAATTTACATATTGTAGTTAAGTCGAGTGTGTATGGAAATTTTAGCC	1800
Qy	1801	ggcgcaaggaggttcgtgaaggctgatatatatctttctattgtgtctattgtatgctg	1860
Db	1801	GGCGCAAGGAGTTCGTGAAGCTGTATATATTTTCTTTATTGTGTATTTGTATTCG	1860
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Db	1921	CAC TTCAGTTCAGGCTGAAATTCATTAACATATTATTTAAACAAATGTGATGTGACTA	1980
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Qy	2221	ggttctgcccataactagtaataaaactctcgtaaatattatgggaaaaagaaggtcccttt	2280
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Db	2401	ATAGTTAAACGATTAAAGATTATTCGATTTCGATTTAAAAATTCGATTAGCGATTGTCGCTG	2460
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Qy	2521	ttagtaaatgtagtgacgcttttaatttttaaaaaagaatgtctactcgaagaattaaatcc	2580
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Db	2581	AGGAATTTGTAACAGTTATGGAAATGTATGAAGAAATCAACAAATTAATACCGAACCAAGG	2640
Qy	2641	tagactagggttagcatcaggagatgaaattaaaaacaataattaggaccgacttaaatgg	2700
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Qy	2701	aacttgcgaggttattgataaaccttttttaatttaaaaaactcattgtcattaatggsgaa	2760
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Qy	2761	taactttgtatctctgatacgaataagctcacttaactatcgatagcgtaattata	2820
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Qy	2821	actgttagtatatcgatatggggagtagtcactagcatcagaataagtcattatagga	2880
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Db	2881	ATCGGTTGTGTTTAATGTTATGCTTACCGAATAATTTACAAATGCTGTGTGATACACTAAC	2940
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Db	3001	AAATTTTGAAGAAAAAATGATAAATGTAATACAGATAATTGCGGTGTGTATTGTATAT	3029
RESULT	2		
LOCUS	AF143846	3629 bp	mrna INV 27-MAY-1999
DEFINITION	Heliothis virescens putative nicotinic acetylcholine receptor alpha 7-1 subunit mRNA, complete cds.		
ACCESSION	AF143846		
NID	94895004		
VERSION	AF143846.1	GI:4895004	
KEYWORDS	tobacco budworm.		
SOURCE	Heliothis virescens		
ORGANISM	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Diptysia; Noctuidae; Noctuidae; Heliothinae; Heliothis.		
REFERENCE	1 (bases 1 to 3629)		
AUTHORS	Schulte, T., Oellers, N. and Adamczewski, M.		
TITLE	Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce1 than to other insect nicotinic acetylcholine receptor alpha subunits		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3629)		
AUTHORS	Schulte, T., Oellers, N. and Adamczewski, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-APR-1999) ZF-BTB, Bayer AG, Bldg. Q 18., Leverkusen 51368, Germany		
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ORIGIN	1 others		

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Db 3001 AAATTTTAGAAAAAATAAAAAAATAAAAAA 3029

## RESULT 2

BYRNAEF2 3001 bp mRNA PLN  
LOCUS Beta vulgaris cDNA for elongation factor 2. 01-SEP-1997  
DEFINITION 297178  
ACCESSION 92369713  
NID 297178.1 GI:2369713  
VERSION elongation factor 2.  
KEYWORDS beet.  
SOURCE Beta vulgaris  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Caryophyllales; Caryophyllaceae; Chenopodiaceae; Beta.  
REFERENCE 1 (bases 1 to 3001)  
AUTHORS Vogel, R.  
TITLE Direct Submission  
JOURNAL Submitted (23-JUN-1997) Vogel R., Botanisches Institut, Universitaet Heidelberg, Im Neuenheimer Feld 360, 69120 Heidelberg GERMANY  
REFERENCE 2 (bases 1 to 3001)  
AUTHORS Vogel, R. and Rausch, T.  
JOURNAL Unpublished  
FEATURES Location/Qualifiers  
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CDS

Thu Jan 20 07:42:09 2000

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BASE COUNT 739 a 623 c 776 g 863 t

Query Match 3.2%; Score 99; DB 7; Length 3001;  
Best Local Similarity 100.0%; Pred. No. 8.9e-43;  
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Db 2963 TCCACCGGTGGGTACAGTAAGTGTACCAATTCG 3001

MLT 3

LOCUS AF045432 2873 bp mRNA VET 18-MAR-1998  
DEFINITION Danio rerio stem cell leukemia protein (tal-1) mRNA, complete cds.  
ACCESSION AF045432  
NID 92921800  
VERSION AF045432.1 GI:2921800  
KEYWORDS zebrafish.  
SOURCE Danio rerio.  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprinidae; Rasbora; Danio.

REFERENCE 1 (bases 1 to 2873)  
AUTHORS Liao, E.C., Paw, B.H., Oates, A.C., Pratt, S.J., Postlethwait, J.H. and Zon, L.I.  
TITLE SCL/Tal-1 transcription factor acts downstream of cloche to specify hematopoietic and vascular progenitors in zebrafish  
JOURNAL Genes Dev. 12 (5), 621-626 (1998)  
MEDLINE 98167906  
REFERENCE 2 (bases 1 to 2873)  
AUTHORS Liao, E.C., Paw, B.H., Oates, A.C., Pratt, S.J., Postlethwait, J.H. and Zon, L.I.

DIRECT SUBMISSION  
SUBMITTED (30-JAN-1998) Hematology/Oncology, Harvard Medical School, 300 Longwood Avenue, Boston, MA 02115, USA

LOCATION/QUALIFIERS  
1. .2873  
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gene

CDS  
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BASE COUNT 799 a 661 c 639 g 714 t

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Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 3072 caccgggtgggtaccaggtaagtgtaccacaa 3104  
Db 2841 CACCGGTGGGTACAGTAAGTGTACCCAA 2873

RESULT 4

LOCUS MMU39066 2015 bp mRNA ROD 12-JUL-1996  
DEFINITION Murine MAP kinase kinase 6c mRNA, complete cds.  
ACCESSION U39066  
NID 91209674  
VERSION U39066.1 GI:1209674  
KEYWORDS house mouse.  
SOURCE Mus musculus.  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1519)  
AUTHORS Han, J., Lee, J.D., Jiang, Y., Li, Z., Feng, L. and Ulevitch, R.J.  
TITLE Characterization of the structure and function of a novel MAP kinase kinase (MKK6)  
JOURNAL J. Biol. Chem. 271 (6), 2886-2891 (1996)  
MEDLINE 96216353  
REFERENCE 2 (bases 1 to 2015)  
AUTHORS Han, J.  
TITLE Direct Submission  
SUBMITTED (23-OCT-1995) Jiahuai Han, Immunology, The Scripps Research Institute, 10666 N. Torrey Pines Rd., La Jolla, CA 92037, USA

FEATURES  
source

CDS

1. .2015  
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QY 3070 tccaccgggtgggtaccaggtaagtgtac 3099  
Db 1986 TCCACCGGTGGGTACAGTAAGTGTAC 2015

RESULT 5

LOCUS HSU48696 2370 bp mRNA PRI 13-JUL-1996  
DEFINITION Human mariner-like element-containing mRNA, clone pchMT1.  
ACCESSION U48696

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LOCUS	AF045432	2873 bp mRNA
DEFINITION	Danio rerio, stem cell leukemia protein (tal-1) mRNA, complete cds.	VRT 18-MAR-1998
ACCESSION	AF045432	
NID	G2921800	
VERSION	AF045432.1	GI:2921800
KEYWORDS		
SOURCE	zebrafish.	
ORGANISM	Danio rerio	
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2 (bases 1 to 2370)  
Kiyosawa, H. and Chance, P.F.  
Direct Submission  
Submitted (07-FEB-1996) Hidenori Kiyosawa, Neurology Research, The Children's Hospital of Philadelphia, 34th & Civic Center Boulevard, Philadelphia, PA 19104, USA  
Location/Qualifiers  
1. .2370  
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OY 3670 ccaccgggtgggtaccag 3689  
Db 2346 CCACC GG GTGGGT ACCAG 2365

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DEFINITION Z971178  
ACCESSION Z971178  
MID Z971178.1 GI:2369713  
VERSION elongation factor 2.  
KEYWORDS beet.  
SOURCE Beta vulgaris  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euryhallophytes; Spermatophyta; Magnoliophyta; euclitidons; Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.

REFERENCE  
AUTHORS Vogel,R.  
TITLE Direct Submission  
JOURNAL Submitted (23-JUN-1997) Vogel R., Botanisches Institut, Universitaet Heidelberg, Im Neuenheimer Feld 360, 69120 Heidelberg GERMANY

2 (bases 1 to 3001)  
Vogel,R. and Rausch,T.  
Unpublished Location/Qualifiers  
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CDS

Thu Jan 20 07:41:56 2000

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model  
Run on: January 18, 2000, 21:00:23 : Search time 3378.13 Seconds  
(without alignments)  
4683.317 Million cell updates/sec

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Database: GenEmbl.\*  
Word size: 0

Number of hits that pass the threshold : 1561122

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- 3: gb\_cm.\*
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- 6: gb\_ph.\*
- 7: gb\_pl1.\*
- 8: gb\_pl2.\*
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- 10: gb\_pr2.\*
- 11: gb\_pr3.\*
- 12: gb\_ro.\*
- 13: gb\_sy.\*
- 14: gb\_un.\*
- 15: gb\_v1.\*
- 16: gb\_v2.\*
- 17: em\_fun.\*
- 18: em\_hgt.\*
- 19: em\_hum1.\*
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- 21: em\_in.\*
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- 34: gb\_hgt.\*
- 35: gb\_in1.\*
- 36: gb\_in2.\*
- 37: em\_ba1.\*
- 38: em\_ba2.\*
- 39: em\_hum3.\*
- 40: em\_hum4.\*
- 41: gb\_pr4.\*
- 42: gb\_hgt3.\*
- 43: gb\_hgt4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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4	405.6	11.0	1876	11	HSU62436	U62436 Human nicot
5	405.2	11.0	1876	5	AR055255	AR055255 Sequence
6	404.6	10.9	3030	12	S53987	S53987 nicotinic r
7	404	10.9	1509	9	HSNACHRA7	Y08420 H.sapiens m
8	403	10.9	2087	9	HSARA7A	X70297 H.sapiens m
9	401.8	10.9	2106	12	RATNARAD	L31619 Rattus ratt
10	400.8	10.8	1977	10	HSU40583	U40583 Human alpha
11	397.6	10.7	1555	9	HSCHRNA7A	223141 H.sapiens C
12	396.4	10.7	1551	3	BSA7	X93604 B.taurus mr
13	396	10.7	1559	10	HUMATNAR	L25827 Human a7 ni
14	345.6	9.3	2067	35	HVNACHRA1	AJ000399 Heliothis
15	333.4	9.0	2037	4	GGNARA7A	X68586 G.gallus mr
16	327.4	8.8	2696	4	GGN7NAREC	X52295 Chicken alp
17	325.6	8.8	1963	35	SGNARAL1	X55439 S. gregaria
18	324.4	8.8	1578	35	LMNACHRA2	AJ000391 Locusta m
19	312.2	8.4	2090	4	GA8NAREC	X52296 Chicken alp
20	311.8	8.4	1623	35	LMNACHRA3	AJ000392 Locusta m
21	309.2	8.4	2277	5	AR037435	AR037435 Sequence
22	309.2	8.4	1590	10	HSY16281	Y16281 Homo sapien
23	309.2	8.4	2664	11	HSU62431	U62431 Human nicot
24	299	8.1	1908	11	HSU62432	U62432 Human nicot
25	295.8	8.0	1824	35	MSNARALPH	L35901 Human nicot
26	295.4	8.0	1756	5	AR055253	X08795 M.sexta mrn
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31	293.6	7.9	2448	11	HSU62437	X53179 Human mrna
32	293.6	7.9	2068	5	AR055252	U62437 Human nicot
33	292.8	7.8	1512	9	HSNACHRA3A	AR055252 Sequence
34	288.2	7.8	1836	11	AF037646	Y08418 H.sapiens m
35	288	7.8	1833	9	HSNACHRA4G	AF037646 Homo sapi
36	286.2	7.7	1833	9	HSNACHRA4	X87629 H.sapiens m
37	285.6	7.7	3618	3	BTACHRA1	X02509 B.taurus mr
38	285.2	7.7	1910	10	HUMNAR	X37981 Human alpha
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40	284.6	7.7	1884	9	HSNACHRA4	Y08421 H.sapiens m
41	284.4	7.7	1860	12	MUSACHRA8	M17640 Mus musculu
42	281.8	7.6	1521	5	AR037436	AR037436 Sequence
43	280.8	7.6	2838	35	DMNARAS	Y15593 Drosophila
44	280.6	7.6	1584	41	HUMA3NARSP	M86383 Homo sapien
45	280.4	7.6	2374	5	AR055254	AR055254 Sequence

ALIGNMENTS

RESULT 1

AF143846

LOCUS

DEFINITION

ACCESSION

NID

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AF143846 3629 bp mRNA INV 27-MAY-1999  
Heliothis virescens putative nicotinic acetylcholine receptor alpha  
7-1 subunit mRNA, complete cds.

AF143846  
94895004  
AF143846.1 GI:4895004  
tobacco budworm.  
Heliothis virescens  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;  
Ditrysia; Noctuoidea; Noctuidae; Heliothinae; Heliothis.

1 (bases 1 to 3629)  
Schulze, T., Oellers, N. and Adamczewski, M.  
Putative alpha subunits of insect nicotinic acetylcholine receptors  
more similar to vertebrate alpha 7 subunits and C. elegans Ce21  
than to other insect nicotinic acetylcholine receptor alpha



subunits  
Unpublished  
2 (bases 1 to 3629)  
Schulte, T., Oellers, N. and Adamczewski, M.  
Direct Submission  
Submitted (19-APR-1999) 2F-BTB, Bayer AG, Bldg. Q 18., Leverkusen  
51368, Germany

FEATURES  
Location/Qualifiers  
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DIWPFDPORCEMKFGSWYDGYQLDLQDEGGDISSFVTNGEWELIGVPGKNE  
IYNCCPEPIDITFAVIRKRLIYFFNLIVPCVLIASHALLGTLPLPDSEKLSLG  
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BASE COUNT 880 a 931 c 922 g 895 t 1 others

Query Match 97.8%; Score 3617; DB 36; Length 3629;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3628; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy 61 gctgtactcacacacatccctccgagcagtagcgatgttgagagatcgacggcac 120  
Dbb 61 GCCGTGACTCCACACATCCCTCCGCGCAGTAGGCGATGTTGAGGATCGGACGGCAC 120

Qy 121 gcgtggcgctgcggcgagcggtcgtaacaaagtgtacacatgaaacacgtaaaagat 180  
b 121 GCGTGGCGCTCGCGAGCGGTGTAACAAAGTTGCATACATATGAAACCGTAAAGAT 180

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Dbb 181 TGAATTTTAAGCCGATCGTGTTCGATAGATCTCTAATAGAGAAGCGGAGTCCGCGCTTG 240

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Dbb 661 AGTGCCACCCACAGACTATGGAACACAGACGCTCTTATGTACACAGCGCGGACGAAGG 720  
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Thu Jan 20 07:41:56 2000

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## RESULT 2

AF143847

LOCUS

DEFINITION

ACCESSION

NID

VERSION

KEYWORDS

SOURCE

ORGANISM

AF143847

3029 bp

mrna

INV

27-MAY-1999

Heliothis virescens putative

7-2 subunit mRNA, complete cds.

AF143847

94895006

AF143847.1

GI:4895006

tobacco budworm.

Heliothis virescens

GenCore version 4.5  
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: January 18, 2000, 21:13:21 : Search time 3378.35 Seconds  
3652.749 Million cell updates/sec

Title: US-09-303-232-1  
Perfect score: 2886  
Sequence: 1 ggcacgagaaagtgttgg.....aaaaaaaaaaaaaaaaaaaaa 2886

Scoring table: OLIGO\_NUC  
Searched: 780561 seqs, 2137953050 residues  
Database : GenEmbl.\*  
Word size : 14

Number of hits that pass the threshold : 99869

- 1: gb\_ba1.\*
- 2: gb\_ba2.\*
- 3: gb\_om.\*
- 4: gb\_ov.\*
- 5: gb\_ph.\*
- 6: gb\_pl1.\*
- 7: gb\_pl2.\*
- 8: gb\_pl3.\*
- 9: gb\_pl4.\*
- 10: gb\_pl5.\*
- 11: gb\_pl6.\*
- 12: gb\_pl7.\*
- 13: gb\_pl8.\*
- 14: gb\_pl9.\*
- 15: gb\_pl10.\*
- 16: gb\_pl11.\*
- 17: gb\_pl12.\*
- 18: gb\_pl13.\*
- 19: gb\_pl14.\*
- 20: gb\_pl15.\*
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- 40: gb\_pl35.\*
- 41: gb\_pl36.\*
- 42: gb\_pl37.\*
- 43: gb\_pl38.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	573	19.9	76947	35	AC004326 Drosophil
C 2	35	1.2	3629	36	AF143846 Heliothis
C 3	31	1.1	355	13	U66809 Asteroech
C 4	31	1.1	41602	42	AC010017 Drosophil
C 5	31	1.1	127189	43	AC010995 Drosophil
C 6	30	1.0	721	9	X73459 H.sapiens m
C 7	30	1.0	442	11	U92988 Homo sapien
C 8	30	1.0	201986	12	AC005289 Mus muscu
C 9	30	1.0	201964	12	MMHC29N7 AF064258 Strongylo
C 10	30	1.0	4552	36	S79891 sr-stripe {
C 11	29	1.0	2782	35	S79891 L04646 Strongyloce
C 12	29	1.0	3568	35	SUSOCTBND L04646 Strongyloce
C 13	29	1.0	4714	36	AF181637 Drosophil
C 14	29	1.0	159507	41	AC004985 Homo sapi
C 15	29	1.0	195098	43	AC007518 Mus muscu
C 16	28	1.0	130663	34	AC007808 Drosophil
C 17	28	1.0	122869	34	AC008895 Homo sapi
C 18	28	1.0	155135	43	AC011087 Homo sapi
C 19	27	0.9	846	8	ATHMGALPH Y14071 Arabidopsis
C 20	27	0.9	162822	11	AC005751 Homo sapi
C 21	27	0.9	199040	34	AC007185 Drosophil
C 22	27	0.9	87585	35	AC004299 Drosophil
C 23	27	0.9	4771	35	DMABDBCLA X51663 D.melanogas
C 24	27	0.9	3885	35	DMABDBP3 X16134 Drosophila
C 25	27	0.9	338234	35	DMU31961 U31961 Drosophila
C 26	27	0.9	80423	35	DROAEDB L07835 Drosophila
C 27	27	0.9	4976	36	DMU19269 U19269 Drosophila
C 28	26	0.9	2508	4	AF032896 AF032896 Petromyzo
C 29	26	0.9	1515	4	CHKVITB M18060 Chicken vit
C 30	26	0.9	5791	4	CHKVITC X13607 Chicken vit
C 31	26	0.9	20343	4	GGVITIG X80212 F.hygrometr
C 32	26	0.9	11132	7	FHRNA M63498 S.yescristia
C 33	26	0.9	4673	7	YSCUGA35 AL023094 Arabidops
C 34	26	0.9	125502	8	ATT4L20 AL112245 Botrytis
C 35	26	0.9	660	8	CNS019Y5 AL114081 Botrytis
C 36	26	0.9	696	8	CNS01BD5 AC006341 Arabidops
C 37	26	0.9	114498	8	F309 AB018516 Homo sapi
C 38	26	0.9	408	9	AB023054 AB023054 Homo sapi
C 39	26	0.9	162383	9	AB023055 Homo sapi
C 40	26	0.9	162383	9	AB023055 Homo sapi
C 41	26	0.9	100000	9	AP000517 Homo sapi
C 42	26	0.9	101817	9	HS1216H12 AL008715 Homo sapi
C 43	26	0.9	114231	9	HS390C10 AL008721 Homo sapi
C 44	26	0.9	114771	9	HS569D19 AL022334 Human DNA
C 45	26	0.9	185001	34	AC007366 AC007366 Homo sapi

ALIGNMENTS

RESULT 1	AC004326/c	AC004326	76947 bp	DNA	INV	01-MAY-1998
LOCUS	Drosophila melanogaster	Drosophila melanogaster	DNA sequence (PI DS05899 (D22)), complete sequence.			
DEFINITION	AC004326 L43425	AC000556	AC001301	AC000557	AC000558	AC000559
ACCESSION	AC000560	AC000561	AC000562	AC000563	AC000564	AC000565
	AC002866	AC002867	L43424	AC002868	L39682	AC002869 L39684 L43423
	AC000566	L39683	AC000567	AC003871		
NID	93097819					
VERSION	AC004326.1	GI:3097819				
KEYWORDS	Drosophila melanogaster (Subclones in Sac from PI clone DS05899 (D22)) DNA.					
SOURCE	Drosophila melanogaster					
ORGANISM	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.					
REFERENCE	1 (bases 1 to 76947)					

## AUTHORS

Celniker, S.E., Aghavani, A., Arcaina, T.T., Baxter, E., Blazet, R.G.,  
Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J.H., Houston, K.A.,  
Hummati, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B.,  
Lomoten, M.A., Mada, P., Mok, M.S., Moshrefi, A.R., Moshrefi, M.,  
Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, D., Snir, E.,  
Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zieran, L.L.  
and Kimmel, B.

## TITLE

Sequencing of Alcohol dehydrogenase region

## JOURNAL

Unpublished (1997)

## REFERENCE

2 (bases 1 to 76947)

## AUTHORS

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## COMMENT

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Sequence submitted by:

Berkeley Drosophila Genome Project

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For further information about this sequence, including its location

and relationship to other sequences, please visit our sequence

archive web site

(http://fruitfly.berkeley.edu/sequence-archive.html) or send email

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